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RAW SEQUENCE LISTING   DATE: 03/22/2002
PATENT APPLICATION: US/10/087,167   TIME: 10:47:24

      Input Set : A:\PTO.VSK.txt
      Output Set: N:\CRF3\03222002\J087167.raw

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  3 <110> APPLICANT: Pascal, Erica
  4        Valentine, Scott
  5        Brown, Jeffrey
  6        Cockrell, Adam
  7        Johnson, Brian
  9 <120> TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 11 <130> FILE REFERENCE: 50018A
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/087,167
C--> 13 <141> CURRENT FILING DATE: 2002-03-01
 13 <150> PRIOR APPLICATION NUMBER: US 60/242,969
 14 <151> PRIOR FILING DATE: 2000-10-24
 16 <160> NUMBER OF SEQ ID NOS: 148
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2840
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Manduca sexta
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (361)..(2031)
 28 <223> OTHER INFORMATION: Manduca sexta Ecdysone Receptor
 31 <300> PUBLICATION INFORMATION:
 32 <301> AUTHORs: Fujiwara, et al.
 33 <302> TITLE: Cloning of an ecdysone receptor homolog from Manduca sexta and the
 34        developmental profile of its mRNA in wings
 35 <303> JOURNAL: Insect Biochem. Mol. Biol.
 36 <304> VOLUME: 25
 37 <305> ISSUE: 7
 38 <306> PAGES: 845-856
 39 <307> DATE: 1995
 40 <308> DATABASE ACCESSION NO: Genbank/U19812
 41 <309> DATABASE ENTRY DATE: 1996-02-03
 43 <400> SEQUENCE: 1
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 48 cttcggattg tgttgtgact gaaaagcgac gcgtatcgtg gtcgaagatt ctctataagt     180
 50 gcataatata ttcgagacag tggatagcga ttcgtttcgg tttcatcgcg cggatgagtg     240
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 54 tacgtcagag gatgtccctc ggtggtcacg gaagccgggg cgtgtgacgc gctcttcgac     360
 56 atg aga cgc cgc tgg tca aac aac gga tgt ttc cct ctg cga atg ttt      408
 57 Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Leu Arg Met Phe
 58 1               5                   10                  15
 60 gag gag agc tcc tct gaa gtg act tct tcc tcg gcg ttc ggg atg ccg      456
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65 Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
66          35              40              45
68 ggc ctc gag ctc tgg agc tac gat gag acc atg aca aac tat ccg gcg       552
69 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
70      50              55              60
72 cag tca ctg ctc ggc gcg tgt aat gcg ccg cag cag cag cag caa cag       600
73 Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln Gln
74 65              70              75              80
76 caa caa cag cag ccg tcc gct cag ccg ctg ccg tct atg ccg ctg ccg       648
77 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
78              85              90              95
80 atg cct cct aca act cct aaa tca gag aac gag tcc atg tcg tca ggt       696
81 Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
82              100             105             110
84 cga gaa gaa tta tca ccg gcc tca agt ata aat gga tgt agt act gat       744
85 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
86          115             120             125
88 ggg gaa cca aga cga cag aag aaa ggg cca gcg ccg cgc cag cag gag       792
89 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
90      130             135             140
92 gaa ctg tgc ctt gtt tgc ggc gac agg gct tcg gga tat cac tat aac       840
93 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
94 145             150             155             160
96 gcg ctt acg tgc gaa gga tgt aaa ggg ttc ttc agg cgg agt gtg acc       888
97 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
98              165             170             175
100 aag aat gcg gta tat att tgt aaa ttt gga cac gcc tgc gag atg gac      936
101 Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp
102             180             185             190
104 atg tac atg agg aga aaa tgc caa gag tgt cgg ttg aag aaa tgc ctc      984
105 Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
106         195             200             205
108 gcg gtg ggc atg agg ccc gag tgc gtc gtc cca gag tcc acg tgc aag      1032
109 Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys
110     210             215             220
112 aac aaa aga aga gaa aag gaa gca cag aga gaa aaa gac aaa ctg cca      1080
113 Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro
114 225             230             235             240
116 gtc agt acg acg aca gtg gac gat cat atg cct gcc ata atg caa tgt      1128
117 Val Ser Thr Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys
118             245             250             255
120 gac cct ccg ccc cca gag gcg gca agg att cac gaa gtg gtc ccg agg      1176
121 Asp Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg
122             260             265             270
124 ttc cta acg gag aag cta atg gag cag aac aga ctg aag aat gtg acg      1224
125 Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr
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PATENT APPLICATION: US/10/087,167

Input Set : A:\PTO.VSK.txt
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129 Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr
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132 cag gag ggg tac gag cag ccg tcg gag gaa gat ctc aag aga gtt aca   1320
133 Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr
134 305                  310                  315                  320
136 cag aca tgg cag tta gaa gaa gaa gaa gag gag gaa act gac atg ccc   1368
137 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro
138                  325                  330                  335
140 ttc cgt cag atc aca gag atg acg atc tta aca gtg cag ctt att gta   1416
141 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val
142                  340                  345                  350
144 gaa ttc gca aag gga cta ccg gga ttc tcc aag ata tct cag tcc gat   1464
145 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp
146         355                  360                  365
148 caa att aca tta tta aag gcg tca tca agc gaa gtg atg atg ctg cga   1512
149 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg
150         370                  375                  380
152 gtg gcg cga cgg tac gac gcg gcg acg gac agc gtg ctg ttc gcg aac   1560
153 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn
154 385                  390                  395                  400
156 aac cag gcg tac acg cgc gac aac tac cgc aag gcg ggc atg tcc tac   1608
157 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr
158                  405                  410                  415
160 gtc atc gag gac ctg ctg cac ttc tgt cgg tgt atg tac tcc atg agc   1656
161 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser
162                  420                  425                  430
164 atg gac aat gtg cac tac gcg ctg ctc acc gcc atc gtt ata ttc tca   1704
165 Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser
166         435                  440                  445
168 gac cgg cca ggc ctc gag caa ccc ctt tta gtg gag gaa atc cag aga   1752
169 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg
170     450                  455                  460
172 tac tac ttg aag acg ctg cgg gtt tac att tta aat cag cac agc gcg   1800.
173 Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala
174 465                  470                  475                  480
176 tcg cct cgc tgc gcc gtg ctg ttc ggc aag atc ctc ggc gtg ctg acg   1848
177 Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr
178                  485                  490                  495
180 gaa ctg cgc acg ctc ggc acg cag aac tcc aac atg tgc atc tcg ctg   1896
181 Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu
182         500                  505                  510
184 aag ctg aag aac agg aaa ctt ccg cca ttc ctc gag gag atc tgg gac   1944
185 Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp
186         515                  520                  525
188 gtg gcc gaa gtg tcg acg acg cag ccg acg ccg ggg gtg gcg gcg cag   1992
189 Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln
190     530                  535                  540
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194 545             550                 555
196 ggcgccgcgc cccgccgccc ccgccgccgc cgctcccccg cgccgccgcc gcgcgccccc   2101
198 gcggcctgcg ctgagtgcgg gacccgcccc gaggagagaa cgctcataga ctggctagtt   2161
200 ttagtgaagt gcacggacgc gatcgtggga ccgcatcgac gcgtccgtga ggacagtgca   2221
202 aatattaccg ctagggccgg ttcgtacgtg tccggtgacc gacgacgatg atgcgcgtga   2281
204 gattagtgaa tatatgtgtt gttgaacgtt tggagagtat atttagtgtt gatcgtcggg   2341
206 agcgcgcggc cggcgcgtgt cggcgagctg tccgccgcgc gccggccgcg gcgactccgc   2401
208 gttttttttcg tttgcgaccg gaaaccgagt cggtcactcg gatacgcccg tatgataaga  2461
210 cttctttcga taaataagtt cacctgtatt gcgcgtacat acgagaatta taaagaaaaa   2521
212 aagtaatata tgaagagatg tttctattgg gtgaaaagtt taaacttatg tttatttacc   2581
214 aaaattaact atacgttgat cgaccttttg actataatat tgtgctgggt cgttggcagc   2641
216 ggccgacgaa cgcgcgccga ccatatttgt ttatatatag tttatgtgag acgttatcgt   2701
218 gtcgtgtcca cttagttccg attcatgttc caccaggtcg gtgtagtgat cagggcgggc   2761
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226 <211> LENGTH: 556
227 <212> TYPE: PRT
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230 <400> SEQUENCE: 2

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237             20                  25                  30
240 Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
241         35                  40                  45
244 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
245     50                  55                  60
248 Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln Gln
249 65                  70                  75                  80
252 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
253                 85                  90                  95
256 Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
257             100                 105                 110
260 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
261         115                 120                 125
264 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
265     130                 135                 140
268 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
269 145                 150                 155                 160
272 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
273                 165                 170                 175
276 Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp
277             180                 185                 190
280 Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
281         195                 200                 205
284 Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys
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Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\03222002\J087167.raw

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285     210                 215                 220
288 Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro
289 225                 230                 235                 240
292 Val Ser Thr Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys
293                 245                 250                 255
296 Asp Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg
297                 260                 265                 270
300 Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr
301                 275                 280                 285
304 Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr
305         290                 295                 300
308 Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr
309 305                 310                 315                 320
312 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro
313                 325                 330                 335
316 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val
317             340                 345                 350
320 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp
321         355                 360                 365
324 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg
325     370                 375                 380
328 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn
329 385                 390                 395                 400
332 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr
333                 405                 410                 415
336 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser
337     .           420                 425                 430
340 Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser
341         435                 440                 445
344 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg
345     450                 455                 460
348 Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala
349 465                 470                 475                 480
352 Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr
353                 485                 490                 495
356 Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu
357             500                 505                 510
360 Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp
361         515                 520                 525
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369 545                 550                 555
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375 <213> ORGANISM: Ostrinia nubilalis
377 <220> FEATURE:
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VERIFICATION SUMMARY   DATE: 03/22/2002
PATENT APPLICATION: **US/10/087,167**   TIME: 10:47:25

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Output Set: **N:\CRF3\03222002\J087167.raw**

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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/087,167**

DATE: 03/22/2002
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